

## SEQUENCE LISTING

&lt;110&gt; Lukyanov, Sergey

&lt;120&gt; FLUORESCENT PROTEINS FROM COPEPODA SPECIES AND METHODS FOR USING SAME

&lt;130&gt; COP\_TEXT.DOC

&lt;160&gt; 30

&lt;170&gt; PatentIn version 3.1

&lt;210&gt; 1

&lt;211&gt; 1010

&lt;212&gt; DNA

&lt;213&gt; Pontellina plumata

&lt;400&gt; 1

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gcagggttat tggggatttc aagggttgctg ggacaggatt ccttgaggac agtgtgatct      420
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&lt;210&gt; 2

&lt;211&gt; 222

&lt;212&gt; PRT

&lt;213&gt; Pontellina plumata

&lt;400&gt; 2

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Met Pro Ala Met Lys Ile Glu Cys Arg Ile Ser Gly Thr Leu Asn Gly
1           5           10           15
Val Val Phe Glu Leu Val Gly Gly Gly Glu Gly Ile Pro Glu Gln Gly
          20           25           30

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Arg Met Thr Asn Lys Met Lys Ser Thr Lys Gly Ala Leu Thr Phe Ser  
 35 40 45  
 Pro Tyr Leu Leu Ser His Val Met Gly Tyr Gly Phe Tyr His Phe Gly  
 50 55 60  
 Thr Tyr Pro Ser Gly Tyr Glu Asn Pro Phe Leu His Ala Ala Asn Asn  
 65 70 75 80  
 Gly Gly Tyr Thr Asn Thr Arg Ile Glu Lys Tyr Glu Asp Gly Gly Val  
 85 90 95  
 Leu His Val Ser Phe Ser Tyr Arg Tyr Glu Ala Gly Arg Val Ile Gly  
 100 105 110  
 Asp Phe Lys Val Val Gly Thr Gly Phe Pro Glu Asp Ser Val Ile Phe  
 115 120 125  
 Thr Asp Lys Ile Ile Arg Ser Asn Ala Thr Val Glu His Leu His Pro  
 130 135 140  
 Met Gly Asp Asn Val Leu Val Gly Ser Phe Ala Arg Thr Phe Ser Leu  
 145 150 155 160  
 Arg Asp Gly Gly Tyr Tyr Ser Phe Val Val Asp Ser His Met His Phe  
 165 170 175  
 Lys Ser Ala Ile His Pro Ser Ile Leu Gln Asn Gly Gly Ser Met Phe  
 180 185 190  
 Ala Phe Arg Arg Val Glu Glu Leu His Ser Asn Thr Glu Leu Gly Ile  
 195 200 205  
 Val Glu Tyr Gln His Ala Phe Lys Thr Pro Thr Ala Phe Ala  
 210 215 220

<210> 3

<211> 1010

<212> DNA

<213> *Pontellina plumata*

<400> 3

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tgaccacat cagacgaaga acttgattct aagattatat gaattttca aaaaaacaat      960
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<210> 4

<211> 222

<212> PRT

<213> Pontellina plumata

<400> 4

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Met Pro Ala Met Lys Ile Glu Cys Arg Ile Thr Gly Thr Leu Asn Gly
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Val Glu Phe Glu Leu Val Gly Gly Gly Glu Gly Thr Pro Glu Gln Gly
          20           25           30
Arg Met Thr Asn Lys Met Lys Ser Thr Lys Gly Ala Leu Thr Phe Ser
          35           40           45
Pro Tyr Leu Leu Ser His Val Met Gly Tyr Gly Phe Tyr His Phe Gly
          50           55           60
Thr Tyr Pro Ser Gly Tyr Glu Asn Pro Phe Leu His Ala Ile Asn Asn
65           70           75           80
Gly Gly Tyr Thr Asn Thr Arg Ile Glu Lys Tyr Glu Asp Gly Gly Val
          85           90           95
Leu His Val Ser Phe Ser Tyr Arg Tyr Glu Ala Gly Arg Val Ile Gly
          100          105          110
Asp Phe Lys Val Val Gly Thr Gly Phe Pro Glu Asp Ser Val Ile Phe
          115          120          125
Thr Asp Lys Ile Ile Arg Ser Asn Ala Thr Val Glu His Leu His Pro
          130          135          140
Met Gly Asp Asn Val Leu Val Gly Ser Phe Ala Arg Thr Phe Ser Leu
145          150          155          160
Arg Asp Gly Gly Tyr Tyr Ser Phe Val Val Asp Ser His Met His Phe
          165          170          175
Lys Ser Ala Ile His Pro Ser Ile Leu Gln Asn Gly Gly Pro Met Phe
          180          185          190
Ala Phe Arg Arg Val Glu Glu Leu His Ser Asn Thr Glu Leu Gly Ile
          195          200          205

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Val Glu Tyr Gln His Ala Phe Lys Thr Pro Ile Ala Phe Ala

210

215

220

<210> 5

<211> 814

<212> DNA

<213> Labidocera aestiva

<400> 5

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gatggaaaca ctgatgaagg acgtatgacc aacaagatga agtccaccaa aggacctctc      180
tccctctctc cctacctact ctcccacatc atgggctacg gattctatca ctatgctacc      240
ttccctgctg gatatgagaa tgtctacctc catgctgcta agaattggagg ctacaccaac      300
accaggactg agaggtaaga agacggagga atcatttcgg tcaacttcac ctacagatat      360
gagggaaaca aggttatcgg agacttcaag gttgttggat caggattccc agctaacagt      420
gttatcttca ctgacaagat catcaagtcc aacccaacct gtgagcacat ctacccaag      480
ggagataata tctttgtcaa tgcctacact cgaacttggg tgcctgagaga tggaggatac      540
tactctgcac aggtcaacaa tcctctccac ttcaagactg ccatgcaccc caccatgctc      600
cagaacggag gatccatgtt tacctacagg aaggttgagg agctccacag ccagtcagat      660
gttggtattg tagaatacca acatgtcttc aagaccccaa ctgcttttgc ctaagcttgg      720
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<210> 6

<211> 222

<212> PRT

<213> Labidocera aestiva

<400> 6

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Met Pro Val Met Lys Ile Glu Cys Arg Ile Ser Gly Thr Met Asn Gly
1           5           10           15
Glu Glu Phe Glu Leu Val Gly Ala Gly Asp Gly Asn Thr Asp Glu Gly
          20           25           30
Arg Met Thr Asn Lys Met Lys Ser Thr Lys Gly Pro Leu Ser Phe Ser
          35           40           45
Pro Tyr Leu Leu Ser His Ile Met Gly Tyr Gly Phe Tyr His Tyr Ala
          50           55           60
Thr Phe Pro Ala Gly Tyr Glu Asn Val Tyr Leu His Ala Ala Lys Asn
65           70           75           80

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Gly Gly Tyr Thr Asn Thr Arg Thr Glu Arg Tyr Glu Asp Gly Gly Ile  
                     85                    90                    95  
 Ile Ser Val Asn Phe Thr Tyr Arg Tyr Glu Gly Asn Lys Val Ile Gly  
                     100                    105                    110  
 Asp Phe Lys Val Val Gly Ser Gly Phe Pro Ala Asn Ser Val Ile Phe  
                     115                    120                    125  
 Thr Asp Lys Ile Ile Lys Ser Asn Pro Thr Cys Glu His Ile Tyr Pro  
                     130                    135                    140  
 Lys Gly Asp Asn Ile Leu Val Asn Ala Tyr Thr Arg Thr Trp Met Leu  
 145                    150                    155                    160  
 Arg Asp Gly Gly Tyr Tyr Ser Ala Gln Val Asn Asn His Leu His Phe  
                     165                    170                    175  
 Lys Thr Ala Met His Pro Thr Met Leu Gln Asn Gly Gly Ser Met Phe  
                     180                    185                    190  
 Thr Tyr Arg Lys Val Glu Glu Leu His Ser Gln Ser Asp Val Gly Ile  
                     195                    200                    205  
 Val Glu Tyr Gln His Val Phe Lys Thr Pro Thr Ala Phe Ala  
                     210                    215                    220

<210> 7  
 <211> 753  
 <212> DNA  
 <213> cf. *Pontella meadi* Wheeler  
 <400> 7

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 atacagatga gggacgcatg accaacaataa tgaagtccat caaaggacct atctccttct 180  
 ctccctacct cctctccac attcttggtc acgggatatta ccactttgca accctccctg 240  
 ctggatatga aaatatctac ctccatgcca tgaagaatgg aggttactcc aatgtcagaa 300  
 ctgagaggta tgaggatgga ggcctcattt ctataacctt caactacaga tatgaaggga 360  
 acaagatcat tggagacttc aaggttggtg gaacaggatt ccctaccaac agtcttatct 420  
 tcactgacaa gatcattaaa tccaacccta cctgtgagaa catgttcccc aaggctgaca 480  
 atactcttgt gaatgcctac accagaacat atttgcttaa agatgggtgga tactactctg 540  
 cccagggtta caaccatctg cacttcaaga gtgccatcca taccaccatg ctccagaatg 600  
 gcggatccat gttcacctac agagttgtag aggagacaca cactcagaac gaagttgcta 660  
 ttgtagagta ccaaaatgtc tccaaaactc caactgcgtt tgcttgaaat acttgtaata 720  
 aaactgcaaa gaaataaact aaattgtaca atc 753

<210> 8  
 <211> 222

<212> PRT

<213> cf. Pontella meadi Wheeler

<400> 8

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Met Pro Asp Met Lys Leu Glu Cys His Ile Ser Gly Thr Met Asn Gly
1           5           10           15
Glu Glu Phe Glu Leu Ile Gly Ala Gly Asp Gly Asn Thr Asp Glu Gly
20           25           30
Arg Met Thr Asn Lys Met Lys Ser Ile Lys Gly Pro Ile Ser Phe Ser
35           40           45
Pro Tyr Leu Leu Ser His Ile Leu Gly Tyr Gly Tyr Tyr His Phe Ala
50           55           60
Thr Phe Pro Ala Gly Tyr Glu Asn Ile Tyr Leu His Ala Met Lys Asn
65           70           75           80
Gly Gly Tyr Ser Asn Val Arg Thr Glu Arg Tyr Glu Asp Gly Gly Ile
85           90           95
Ile Ser Ile Thr Phe Asn Tyr Arg Tyr Glu Gly Asn Lys Ile Ile Gly
100          105          110
Asp Phe Lys Val Val Gly Thr Gly Phe Pro Thr Asn Ser Leu Ile Phe
115          120          125
Thr Asp Lys Ile Ile Lys Ser Asn Pro Thr Cys Glu Asn Met Phe Pro
130          135          140
Lys Ala Asp Asn Thr Leu Val Asn Ala Tyr Thr Arg Thr Tyr Leu Leu
145          150          155          160
Lys Asp Gly Gly Tyr Tyr Ser Ala Gln Val Asn Asn His Met His Phe
165          170          175
Lys Ser Ala Ile His Thr Thr Met Leu Gln Asn Gly Gly Ser Met Phe
180          185          190
Thr Tyr Arg Val Val Glu Glu Thr His Thr Gln Asn Glu Val Ala Ile
195          200          205
Val Glu Tyr Gln Asn Val Phe Lys Thr Pro Thr Ala Phe Ala
210          215          220

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<210> 9

<211> 880

<212> DNA

<213> cf. Pontella meadi Wheeler

<400> 9

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tcaaaatgcc tgacatgaag cttgagtgcc acatctccgg aaccatgaat ggagaggagt 180  
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 agtccatcaa aggacctctc tccctctctc cctacctact cteccacatt cttggctatg 300  
 gatattacca ctttgcaacc ttcctgctg gatatgaaa tatctacct catgccatga 360  
 agaatggagg ttactcaaat gtcaggactg agaggatga ggatggaggc atcatttcta 420  
 taaccttcaa ctacagatat gaaggcagca agatcattgg agacttcaaa gttattggaa 480  
 caggattccc taccgacagt cttatcttca ctgacaagat cattaaatcc aacctacct 540  
 gcgagaacat gttccccaag gctgacaaca ttcttgtgaa tgcctacacc agaacctatt 600  
 tgcttaaaaga tgggtggatac tactctgccc aggttaacaa ccatatgcac ttcaagagtg 660  
 ccatccatcc tacaatgctc cagaatggtg gatccatgtt cactcacaga gtagtagagg 720  
 agaaccacac taagaccaac gttgctatcg tagagtacca aaatgtcttc aaaactccta 780  
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 gcattttatt aatgcataga aaaataaatg tatattttat 880

<210> 10

<211> 222

<212> PRT

<213> cf. *Pontella meadi* Wheeler

<400> 10

Met	Pro	Asp	Met	Lys	Leu	Glu	Cys	His	Ile	Ser	Gly	Thr	Met	Asn	Gly
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Glu	Glu	Phe	Glu	Leu	Ile	Gly	Ser	Gly	Asp	Gly	Asn	Thr	Asp	Gln	Gly
			20					25					30		
Arg	Met	Thr	Asn	Asn	Met	Lys	Ser	Ile	Lys	Gly	Pro	Leu	Ser	Phe	Ser
			35					40					45		
Pro	Tyr	Leu	Leu	Ser	His	Ile	Leu	Gly	Tyr	Gly	Tyr	Tyr	His	Phe	Ala
			50				55				60				
Thr	Phe	Pro	Ala	Gly	Tyr	Glu	Asn	Ile	Tyr	Leu	His	Ala	Met	Lys	Asn
65				70					75					80	
Gly	Gly	Tyr	Ser	Asn	Val	Arg	Thr	Glu	Arg	Tyr	Glu	Asp	Gly	Gly	Ile
				85					90					95	
Ile	Ser	Ile	Thr	Phe	Asn	Tyr	Arg	Tyr	Glu	Gly	Ser	Lys	Ile	Ile	Gly
			100						105					110	
Asp	Phe	Lys	Val	Ile	Gly	Thr	Gly	Phe	Pro	Thr	Asp	Ser	Leu	Ile	Phe
			115					120					125		
Thr	Asp	Lys	Ile	Ile	Lys	Ser	Asn	Pro	Thr	Cys	Glu	Asn	Met	Phe	Pro
			130				135					140			
Lys	Ala	Asp	Asn	Ile	Leu	Val	Asn	Ala	Tyr	Thr	Arg	Thr	Tyr	Leu	Leu
145				150						155				160	

Lys Asp Gly Gly Tyr Tyr Ser Ala Gln Val Asn Asn His Met His Phe  
                     165                    170                    175  
 Lys Ser Ala Ile His Pro Thr Met Leu Gln Asn Gly Gly Ser Met Phe  
                     180                    185                    190  
 Thr His Arg Val Val Glu Glu Asn His Thr Lys Thr Asn Val Ala Ile  
                     195                    200                    205  
 Val Glu Tyr Gln Asn Val Phe Lys Thr Pro Thr Ala Phe Ala  
                     210                    215                    220

<210> 11  
 <211> 847  
 <212> DNA  
 <213> *Pontella mediterranea*  
 <400> 11

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tttgaacttg ttggtgctgg agaaggaaac actgatgagg gacgcatgac caacaagatg      180
aagtccacca agggacctct ttccttctct ccttatttgc tctcccacgt tcttggttat      240
ggatactacc actatgctac cttccctgct ggatatgaaa atgtctacct ccattgccatg      300
aagaatggag gttactccaa cacaagaact gagaggatg aggatggagg tatcatttct      360
gctacattca actacagata tgaagggaga cagattcatg gagacttcaa ggttgtagga      420
acgggattcc ctgccgacag catcatcttc actgacaaga tcatcaagtc caaccctacc      480
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atgcttagag atggtggata ctactctgcc cagggtcaaca accacatgca ttacagagt      600
gccattcatc ccaccatgct caagaatggt ggatctatgt tcacctacag aaagggttag      660
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actgcttttg ctraattttg taaataaaga aagaatctat aatgcaatag taccttaaag      780
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<210> 12  
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 <212> PRT  
 <213> *Pontella mediterranea*  
 <400> 12

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 Glu Glu Phe Glu Leu Val Gly Ala Gly Glu Gly Asn Thr Asp Glu Gly  
                     20                    25                    30



Arg Met Thr Asn Lys Met Lys Ser Thr Lys Gly Pro Leu Ser Phe Ser  
 35 40 45  
 Pro Tyr Leu Leu Ser His Val Leu Gly Tyr Gly Tyr Tyr His Tyr Ala  
 50 55 60  
 Thr Phe Pro Ala Gly Tyr Glu Asn Val Tyr Leu His Ala Met Lys Asn  
 65 70 75 80  
 Gly Gly Tyr Ser Asn Thr Arg Thr Glu Arg Tyr Glu Asp Gly Gly Ile  
 85 90 95  
 Ile Ser Ala Thr Phe Asn Tyr Arg Tyr Glu Gly Arg Gln Ile His Gly  
 100 105 110  
 Asp Phe Lys Val Val Gly Thr Gly Phe Pro Ala Asp Ser Ile Ile Phe  
 115 120 125  
 Thr Asp Lys Ile Ile Lys Ser Asn Pro Thr Cys Glu His Ile Tyr Pro  
 130 135 140  
 Lys Ala Asn Asn Ile Leu Val Asn Ala Tyr Thr Arg Thr Trp Met Leu  
 145 150 155 160  
 Arg Asp Gly Gly Tyr Tyr Ser Ala Gln Val Asn Asn His Met His Leu  
 165 170 175  
 Gln Ser Ala Ile His Pro Thr Met Leu Lys Asn Gly Gly Ser Met Phe  
 180 185 190  
 Thr Tyr Arg Lys Val Glu Glu Leu His Thr Gln Thr Glu Val Gly Ile  
 195 200 205  
 Val Glu Tyr Gln His Val Phe Lys Arg Pro Thr Ala Phe Ala  
 210 215 220

<210> 13

<211> 850

<212> DNA

<213> *Pontella mediterranea*

<400> 13

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 ttgaaacttg ttggtgctgg agatggaaac actgatgagg gacgcatgac caaccagatg 180  
 aagtcacaaa agggacctct ctcccttctct ccctaattgc tctcccacgt tcttggttat 240  
 ggatactacc actatgctac ctcccttgct ggatatgaaa atgtctccct ccattgocattg 300  
 aagaatggag gttactccaa cacaagaact gagaggatg acgatggagg tatcatttct 360  
 gctaccttca actacagata tgaagggaga cagattcatg gagacttcaa gggtgttgga 420  
 actggattcc ctgccgacag catcatcttc actgacaaga tcatcaagtc caaccctacc 480  
 tgtgagcaca tctaccccaa ggctgacaat attcttgtga atgcctacac cagaacctgg 540  
 atgcttagag atggtggata ctactctgct caggccaaca accacatgca cttaagagt 600

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gccatccatc ccaccatgct ccagaatggt ggatctatgt tcacctacag aaagggttgag 660
gagctccaca cacaaactga agttggtatt gttgagtacc agcatgtttt caagaggccc 720
acagcttttg cttaattttg taaataaaga aagaatttat aatacaatag tgcctttatg 780
tttctaaaac aatgaatgta taaataaatc tcaaaatatt caaaaaaaaa aaaaaaaaaa 840
aaaaaaaaaa 850

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<210> 14
<211> 222
<212> PRT
<213> Pontella mediterranea
<400> 14

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Met Pro His Met Lys Leu Glu Cys Arg Ile Ser Gly Thr Met Asn Gly
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Glu Glu Phe Glu Leu Val Gly Ala Gly Asp Gly Asn Thr Asp Glu Gly
20          25          30
Arg Met Thr Asn Gln Met Lys Ser Thr Lys Gly Pro Leu Ser Phe Ser
35          40          45
Pro Tyr Leu Leu Ser His Val Leu Gly Tyr Gly Tyr Tyr His Tyr Ala
50          55          60
Thr Phe Pro Ala Gly Tyr Glu Asn Val Tyr Leu His Ala Met Lys Asn
65          70          75          80
Gly Gly Tyr Ser Asn Thr Arg Thr Glu Arg Tyr Asp Asp Gly Gly Ile
85          90          95
Ile Ser Ala Thr Phe Asn Tyr Arg Tyr Glu Gly Arg Gln Ile His Gly
100         105         110
Asp Phe Lys Val Val Gly Thr Gly Phe Pro Ala Asp Ser Ile Ile Phe
115         120         125
Thr Asp Lys Ile Ile Lys Ser Asn Pro Thr Cys Glu His Ile Tyr Pro
130         135         140
Lys Ala Asp Asn Ile Leu Val Asn Ala Tyr Thr Arg Thr Trp Met Leu
145         150         155         160
Arg Asp Gly Gly Tyr Tyr Ser Ala Gln Val Asn Asn His Met His Phe
165         170         175
Lys Ser Ala Ile His Pro Thr Met Leu Gln Asn Gly Gly Ser Met Phe
180         185         190
Thr Tyr Arg Lys Val Glu Glu Leu His Thr Gln Thr Glu Val Gly Ile
195         200         205
Val Glu Tyr Gln His Val Phe Lys Arg Pro Thr Ala Phe Ala
210         215         220

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<210> 15  
 <211> 821  
 <212> DNA  
 <213> Unknown  
 <220>  
 <223> nucleic acid sequence for pdae1GFP from an unidentified  
 Pontellidae species, complete cds  
 <400> 15

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tctctccct atcttctctc tcatgtcatg ggatatggat tctatcattt tggaacattt      240
cccagtgggt atgagaatcc ctatgtccac gccatgacga acggtggata taccaacacc      300
aggattgaaa gttatgaaga tggaggtgtt ctttacctta ccttcaacta cagattggat      360
ggaaacaaga ttatcgggga cttcaagtgt gtcggaactg gattccctga ggacagcgtt      420
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gaaaacatca tgaaaaatgc ctacatgaga actctctccc tcagagatgg tggctactac      540
cttggccagg ttaccagcca catccacttc aagaatgcga tccacccatc catccttcat      600
aacggcggat ccattgtcc cttacagaaga gttgaggagc tccacactca aactgatctt      660
ggaattgttg agtaccagca tgtattcaag actcccaactg cttttgcttg aatgccatga      720
agatgaaacc tgaacaagat caatctttat ttaccacaat atgtaaattg ttttaattgta      780
taattctcga gaattcatat aatacataga atttatctta c                                821

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<210> 16  
 <211> 222  
 <212> PRT  
 <213> Unknown  
 <220>  
 <223> amino acid sequence for pdae1GFP from an unidentified Pontellidae  
 species  
 <400> 16

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Met Ala Ala Met Lys Ile Glu Cys Arg Ile Thr Gly Thr Met Asn Gly
1           5           10           15
Val Glu Phe Glu Leu Val Gly Gly Gly Glu Gly Asn Thr Asp Gln Gly
           20           25           30
Arg Met Thr Asn Lys Met Lys Ser Thr Lys Gly Pro Leu Ser Phe Ser
           35           40           45
Pro Tyr Leu Leu Ser His Val Met Gly Tyr Gly Phe Tyr His Phe Gly
           50           55           60

```

Thr Phe Pro Ser Gly Tyr Glu Asn Pro Tyr Val His Ala Met Thr Asn  
 65 70 75 80  
 Gly Gly Tyr Thr Asn Thr Arg Ile Glu Ser Tyr Glu Asp Gly Gly Val  
 85 90 95  
 Leu Tyr Leu Thr Phe Asn Tyr Arg Leu Asp Gly Asn Lys Ile Ile Gly  
 100 105 110  
 Asp Phe Lys Cys Val Gly Thr Gly Phe Pro Glu Asp Ser Val Ile Phe  
 115 120 125  
 Thr Asp Lys Ile Ile Lys Ser Asn Pro Asn Cys Glu His Phe Tyr Pro  
 130 135 140  
 Met Ala Glu Asn Ile Met Lys Asn Ala Tyr Met Arg Thr Leu Ser Leu  
 145 150 155 160  
 Arg Asp Gly Gly Tyr Tyr Ser Gly Gln Val Thr Ser His Ile His Phe  
 165 170 175  
 Lys Asn Ala Ile His Pro Ser Ile Leu His Asn Gly Gly Ser Met Phe  
 180 185 190  
 Thr Tyr Arg Arg Val Glu Glu Leu His Thr Gln Thr Asp Leu Gly Ile  
 195 200 205  
 Val Glu Tyr Gln His Val Phe Lys Thr Pro Thr Ala Phe Ala  
 210 215 220

<210> 17

<211> 669

<212> DNA

<213> Artificial sequence

<220>

<223> nucleic acid sequence for the humanized version of the ppluGFP2

<400> 17

atgcccgcca tgaagatcga gtgccgcac accggcaccc tgaacggcgt ggagttcgag 60  
 ctggtgggag ggggagaggg ccccccgag cagggccgca tgaccaacaa gatgaagagc 120  
 accaagggcg ccccgacatt cagccctac ctgctgagcc acgtgatggg ctacggcttc 180  
 taccacttcg gcaacctacc cagcggctac gagaaccctt tcctgcacgc catcaacaac 240  
 ggcggtctaca ccaacacccg catcgagaag tacgaggacg gcggcgtgct gcacgtgagc 300  
 ttacgtctacc gctacgaggg cggccgcgtg atcggcgact tcaaggtggg gggcacccggc 360  
 ttccccgagg acagcgtgat ctccaccgac aagatcatcc gcagcaacgc caccgtggag 420  
 caccctgcacc ccattgggca taacgtgctg gtgggcagct tcgcccgcac ctccagcctg 480  
 cgcgaaggcg gctactacag ctccgtgggt gacagccaca tgcaattcaa gagcgccatc 540  
 cccccagca tcctgcagaa cgggggcccc atgttcgcct tccgccgcgt ggaggagctg 600  
 cacagcaaca ccgagctggg catcgtggag taccagcacg ccttcaagac cccgatcgca 660  
 ttgcctga 669

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<210> 18
<211> 222
<212> PRT
<213> Artificial sequence
<220>
<223> amino acid sequence for the humanized version of the ppluGFP2
<400> 18
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Met	Pro	Ala	Met	Lys	Ile	Glu	Cys	Arg	Ile	Thr	Gly	Thr	Leu	Asn	Gly
1				5					10					15	
Val	Glu	Phe	Glu	Leu	Val	Gly	Gly	Gly	Glu	Gly	Thr	Pro	Glu	Gln	Gly
			20					25					30		
Arg	Met	Thr	Asn	Lys	Met	Lys	Ser	Thr	Lys	Gly	Ala	Leu	Thr	Phe	Ser
		35					40					45			
Pro	Tyr	Leu	Leu	Ser	His	Val	Met	Gly	Tyr	Gly	Phe	Tyr	His	Phe	Gly
	50					55					60				
Thr	Tyr	Pro	Ser	Gly	Tyr	Glu	Asn	Pro	Phe	Leu	His	Ala	Ile	Asn	Asn
65					70					75				80	
Gly	Gly	Tyr	Thr	Asn	Thr	Arg	Ile	Glu	Lys	Tyr	Glu	Asp	Gly	Gly	Val
				85					90					95	
Leu	His	Val	Ser	Phe	Ser	Tyr	Arg	Tyr	Glu	Ala	Gly	Arg	Val	Ile	Gly
			100					105					110		
Asp	Phe	Lys	Val	Val	Gly	Thr	Gly	Phe	Pro	Glu	Asp	Ser	Val	Ile	Phe
		115					120					125			
Thr	Asp	Lys	Ile	Ile	Arg	Ser	Asn	Ala	Thr	Val	Glu	His	Leu	His	Pro
	130					135					140				
Met	Gly	Asp	Asn	Val	Leu	Val	Gly	Ser	Phe	Ala	Arg	Thr	Phe	Ser	Leu
145					150					155					160
Arg	Asp	Gly	Gly	Tyr	Tyr	Ser	Phe	Val	Val	Asp	Ser	His	Met	His	Phe
				165					170					175	
Lys	Ser	Ala	Ile	His	Pro	Ser	Ile	Leu	Gln	Asn	Gly	Gly	Pro	Met	Phe
			180					185					190		
Ala	Phe	Arg	Arg	Val	Glu	Glu	Leu	His	Ser	Asn	Thr	Glu	Leu	Gly	Ile
		195					200					205			
Val	Glu	Tyr	Gln	His	Ala	Phe	Lys	Thr	Pro	Ile	Ala	Phe	Ala		
	210					215					220				

<210>	19
<211>	589
<212>	DNA
<213>	Artificial sequence

&lt;220&gt;

&lt;223&gt; nucleic acid sequence for the ppluGFP2 with yeast-optimized codon usage

&lt;400&gt; 19

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tactccagaa caaggtagaa tgactaataa aatgaaatct actaaagggtg ctttgacttt      60
ttctccatat ttgttgtctc atggtatggg ttatgggttt tatcattttg gtacttatcc      120
atctgggttat gaaaatccat ttttgcatgc tattaataat ggtgggttata ctaatactag      180
aattgaaaaa catgaagatg gtggtgtttt gcattgttct ttttcttata gatatgaagc      240
tggttagagtt attggcgatt ttaaagtgtt tgggtactgg tttccagaag attctgttat      300
ttttactgat aaaattatta gatctaatac tactgttgaa catttgcac caatgggtga      360
taatgttttg gttgggtctt ttgctagaac tttttcttg agagatgggt gttattattc      420
ttttgttgtt gattctcata tgcattttaa atctgttatt catccatcta ttttgcaaaa      480
tggtgggtcca atgtttgctt ttagaagagt tgaagaattg cattctaata ctgaattggg      540
tattgttgaa tatcaacatg cttttaaaac tccaattgct tttgcttaa      589

```

&lt;210&gt; 20

&lt;211&gt; 222

&lt;212&gt; PRT

&lt;213&gt; Artificial sequence

&lt;220&gt;

&lt;223&gt; amino acid sequence for the ppluGFP2 with yeast-optimized codon usage

&lt;400&gt; 20

```

Met Pro Ala Met Lys Ile Glu Cys Arg Ile Thr Gly Thr Leu Asn Gly
1           5           10          15
Val Glu Phe Glu Leu Val Gly Gly Gly Glu Gly Thr Pro Glu Gln Gly
          20          25          30
Arg Met Thr Asn Lys Met Lys Ser Thr Lys Gly Ala Leu Thr Phe Ser
          35          40          45
Pro Tyr Leu Leu Ser His Val Met Gly Tyr Gly Phe Tyr His Phe Gly
          50          55          60
Thr Tyr Pro Ser Gly Tyr Glu Asn Pro Phe Leu His Ala Ile Asn Asn
65          70          75          80
Gly Gly Tyr Thr Asn Thr Arg Ile Glu Lys Tyr Glu Asp Gly Gly Val
          85          90          95
Leu His Val Ser Phe Ser Tyr Arg Tyr Glu Ala Gly Arg Val Ile Gly
          100         105         110
Asp Phe Lys Val Val Gly Thr Gly Phe Pro Glu Asp Ser Val Ile Phe
          115         120         125

```

Thr Asp Lys Ile Ile Arg Ser Asn Ala Thr Val Glu His Leu His Pro  
 130 135 140  
 Met Gly Asp Asn Val Leu Val Gly Ser Phe Ala Arg Thr Phe Ser Leu  
 145 150 155 160  
 Arg Asp Gly Gly Tyr Tyr Ser Phe Val Val Asp Ser His Met His Phe  
 165 170 175  
 Lys Ser Ala Ile His Pro Ser Ile Leu Gln Asn Gly Gly Pro Met Phe  
 180 185 190  
 Ala Phe Arg Arg Val Glu Glu Leu His Ser Asn Thr Glu Leu Gly Ile  
 195 200 205  
 Val Glu Tyr Gln His Ala Phe Lys Thr Pro Ile Ala Phe Ala  
 210 215 220

<210> 21  
 <211> 669  
 <212> DNA  
 <213> Artificial sequence  
 <220>  
 <223> nucleic acid sequence for the CopCFP mutant  
 <400> 21

atgcccgcca tgaagatcga gtgccgcata accggcaccc tgaacggcgt ggagttcgag 60  
 ctggtggggc gcgagagagg ccccccgag cagggccgca tgaccaacaa gatgaagagc 120  
 accaaaggcg ccccgacctt cagccctac ctgctgagcc acgtgatggg ctggggcttt 180  
 taccacttcg gcacctaccc cagcggtac gagaacctt tcctgcacgc catcaacaac 240  
 ggcggtaca ccaacacccg catcgagaag tacgaggacg gcggcgtgct gcacgtgagc 300  
 ttcagctacc gctacgaggc cggccgcgtg atcggcgact tcaaggtagt gggcacccgc 360  
 ttccccgagg acagcgtgat cttcacccgac aagatcatcc gcagcaacgc caccgtggag 420  
 cacctgcgcc ccatgggcga taacgtgctg gtgggcagct tcgccgcac cttcagcctg 480  
 cgcgacggcg gctactacag cttcgtggtg gacagccaca tgcacttcaa gagcgccatc 540  
 cccccagca tcctgcagaa cgggggcccc atgttcgect tcgccgcgt ggaggagctg 600  
 cacagcaaca ccgagctggg catcgtggag taccagcacg ccttcaagac cccgaccgca 660  
 ttcgcctaa 669

<210> 22  
 <211> 222  
 <212> PRT  
 <213> Artificial sequence  
 <220>  
 <223> amino acid sequence for the CopCFP mutant  
 <400> 22

Met Pro Ala Met Lys Ile Glu Cys Arg Ile Thr Gly Thr Leu Asn Gly  
 1 5 10 15  
 Val Glu Phe Glu Leu Val Gly Gly Gly Glu Gly Thr Pro Glu Gln Gly  
 20 25 30  
 Arg Met Thr Asn Lys Met Lys Ser Thr Lys Gly Ala Leu Thr Phe Ser  
 35 40 45  
 Pro Tyr Leu Leu Ser His Val Met Gly Trp Gly Phe Tyr His Phe Gly  
 50 55 60  
 Thr Tyr Pro Ser Gly Tyr Glu Asn Pro Phe Leu His Ala Ile Asn Asn  
 65 70 75 80  
 Gly Gly Tyr Thr Asn Thr Arg Ile Glu Lys Tyr Glu Asp Gly Gly Val  
 85 90 95  
 Leu His Val Ser Phe Ser Tyr Arg Tyr Glu Ala Gly Arg Val Ile Gly  
 100 105 110  
 Asp Phe Lys Val Val Gly Thr Gly Phe Pro Glu Asp Ser Val Ile Phe  
 115 120 125  
 Thr Asp Lys Ile Ile Arg Ser Asn Ala Thr Val Glu His Leu Arg Pro  
 130 135 140  
 Met Gly Asp Asn Val Leu Val Gly Ser Phe Ala Arg Thr Phe Ser Leu  
 145 150 155 160  
 Arg Asp Gly Gly Tyr Tyr Ser Phe Val Val Asp Ser His Met His Phe  
 165 170 175  
 Lys Ser Ala Ile His Pro Ser Ile Leu Gln Asn Gly Gly Pro Met Phe  
 180 185 190  
 Ala Phe Arg Arg Val Glu Glu Leu His Ser Asn Thr Glu Leu Gly Ile  
 195 200 205  
 Val Glu Tyr Gln His Ala Phe Lys Thr Pro Thr Ala Phe Ala  
 210 215 220

<210> 23

<211> 690

<212> DNA

<213> Artificial sequence

<220>

<223> nucleic acid sequence for the CopGFP-NAl variant

<400> 23

atggagagcg acgagagcgg cctgcccgcg atggagatcg agtgccgcac caccggcacc 60  
 ctgaacggcg tggagtgcga gctggtgggc ggcggagagg gcacccccga gcaggggccgc 120  
 atgaccaaca agatgaagag caccaagggc gccctgacct tcagccocta cctgctgagc 180  
 cacgtgatgg gctacggctt ctaccacttc ggcacctacc ccagcggcta cgagaacccc 240



```

ttcctgcacg ccatacaaca cggcggctac accaacaccc gcacgcagaa gtaacaggac 300
ggcggcgctgc tgcacgtgag cttcagctac cgctacgagg ccggccgcgt gatcggcgac 360
ttcaaggtgg tgggcaccgg cttccccgag gacagcgtga tcttcaccga caagatcctc 420
cgcagcaacg ccaccgtgga gcacctgcac cccatgggcg ataacgtgct ggtgggcagc 480
ttcgcccgca ccttcagcct gcgcgacggc ggctactaca gcttcgtggt ggacagccac 540
atgcacttca agagcgccat ccacccagc atcctgcaga acggggggccc catgttcgcc 600
ttccgcccgcg tggaggagct gcacagcaac accgagctgg gcacgtgga gtaccagcac 660
gccttcaaga ccccgatcgc attcgctga 690

```

<210> 24

<211> 229

<212> PRT

<213> Artificial sequence

<220>

<223> amino acid sequence for the CopGFP-NAL variant

<400> 24

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Met Glu Ser Asp Glu Ser Gly Leu Pro Ala Met Glu Ile Glu Cys Arg
1           5           10           15
Ile Thr Gly Thr Leu Asn Gly Val Glu Phe Glu Leu Val Gly Gly Gly
          20           25           30
Glu Gly Thr Pro Glu Gln Gly Arg Met Thr Asn Lys Met Lys Ser Thr
          35           40           45
Lys Gly Ala Leu Thr Phe Ser Pro Tyr Leu Leu Ser His Val Met Gly
          50           55           60
Tyr Gly Phe Tyr His Phe Gly Thr Tyr Pro Ser Gly Tyr Glu Asn Pro
65           70           75           80
Phe Leu His Ala Ile Asn Asn Gly Gly Tyr Thr Asn Thr Arg Ile Glu
          85           90           95
Lys Tyr Glu Asp Gly Gly Val Leu His Val Ser Phe Ser Tyr Arg Tyr
          100          105          110
Glu Ala Gly Arg Val Ile Gly Asp Phe Lys Val Val Gly Thr Gly Phe
          115          120          125
Pro Glu Asp Ser Val Ile Phe Thr Asp Lys Ile Ile Arg Ser Asn Ala
          130          135          140
Thr Val Glu His Leu His Pro Met Gly Asp Asn Val Leu Val Gly Ser
145          150          155          160
Phe Ala Arg Thr Phe Ser Leu Arg Asp Gly Gly Tyr Tyr Ser Phe Val
          165          170          175
Val Asp Ser His Met His Phe Lys Ser Ala Ile His Pro Ser Ile Leu
          180          185          190

```

Gln Asn Gly Gly Pro Met Phe Ala Phe Arg Arg Val Glu Glu Leu His  
 195 200 205  
 Ser Asn Thr Glu Leu Gly Ile Val Glu Tyr Gln His Ala Phe Lys Thr  
 210 215 220

Pro Ile Ala Phe Ala

225

<210> 25

<211> 819

<212> DNA

<213> Artificial sequence

<220>

<223> nucleic acid sequence for the CopGFP-NA2 variant

<400> 25

```

atgcccgcca tgaagatcga gtgccgcata accggcaccc tgaacggcgt ggagttcgag      60
ctgggtggggcg gcgggagaggg cccccccgag cagggcgcgca tgaccaacaa gatgaagagc      120
accaagggcg ccctgacctt cagcccctac ctgctgagcc acgtgatggg ctacggcttc      180
taccacttcg gcacctaccc cagcggctac gagaaccctt tcctgcacgc catcaacaac      240
ggcgggctaca ccaacacccg catcgagaag tacgaggacg gcggcggtgct gcacgtgagc      300
ttcagctacc gctacgaggc cggcgcgctg atcggcgact tcaaggtggt gggcacccggc      360
ttccccgagg acagcgtgat cttcaccgac aagatcatcc gcagcaacgc caccgtggag      420
cacctgcacc ccattgggca taactgtctg gtgggcagct tcgcccgcac cttcagcctg      480
cgcgacggcg gctactacag cttcgtggtg gacagccaca tgcacttcaa gagcgccatc      540
caccaccagca tcctgcagaa cggggggccc atgttcgcct tcgcgcgcgt ggaggagctg      600
cacagcaaca ccgagctggg catcgtggag taccagcacg ccttcaagac ccgcatcgca      660
ttcgccagat ccagagccca ggccagcaac tcgcgcgtgg atggcacagc cggaccggga      720
tcggccgcga ctctagatca taatcagcca taccacattt gtagagggtt tacttgcttt      780
aaaaaacctc ccacacctcc ccctgaacct gaaacataa      819

```

<210> 26

<211> 272

<212> PRT

<213> Artificial sequence

<220>

<223> amino acid sequence for the CopGFP-NA2 variant

<400> 26

Met Pro Ala Met Lys Ile Glu Cys Arg Ile Thr Gly Thr Leu Asn Gly  
 1 5 10 15

Val	Glu	Phe	Glu	Leu	Val	Gly	Gly	Gly	Glu	Gly	Thr	Pro	Glu	Gln	Gly
			20					25					30		
Arg	Met	Thr	Asn	Lys	Met	Lys	Ser	Thr	Lys	Gly	Ala	Leu	Thr	Phe	Ser
			35				40					45			
Pro	Tyr	Leu	Leu	Ser	His	Val	Met	Gly	Tyr	Gly	Phe	Tyr	His	Phe	Gly
		50				55					60				
Thr	Tyr	Pro	Ser	Gly	Tyr	Glu	Asn	Pro	Phe	Leu	His	Ala	Ile	Asn	Asn
	65					70				75				80	
Gly	Gly	Tyr	Thr	Asn	Thr	Arg	Ile	Glu	Lys	Tyr	Glu	Asp	Gly	Gly	Val
				85					90					95	
Leu	His	Val	Ser	Phe	Ser	Tyr	Arg	Tyr	Glu	Ala	Gly	Arg	Val	Ile	Gly
			100					105					110		
Asp	Phe	Lys	Val	Val	Gly	Thr	Gly	Phe	Pro	Glu	Asp	Ser	Val	Ile	Phe
		115					120					125			
Thr	Asp	Lys	Ile	Ile	Arg	Ser	Asn	Ala	Thr	Val	Glu	His	Leu	His	Pro
		130				135					140				
Met	Gly	Asp	Asn	Val	Leu	Val	Gly	Ser	Phe	Ala	Arg	Thr	Phe	Ser	Leu
	145				150					155					160
Arg	Asp	Gly	Gly	Tyr	Tyr	Ser	Phe	Val	Val	Asp	Ser	His	Met	His	Phe
				165					170					175	
Lys	Ser	Ala	Ile	His	Pro	Ser	Ile	Leu	Gln	Asn	Gly	Gly	Pro	Met	Phe
			180					185					190		
Ala	Phe	Arg	Arg	Val	Glu	Glu	Leu	His	Ser	Asn	Thr	Glu	Leu	Gly	Ile
		195					200						205		
Val	Glu	Tyr	Gln	His	Ala	Phe	Lys	Thr	Pro	Ile	Ala	Phe	Ala	Arg	Ser
		210					215					220			
Arg	Ala	Gln	Ala	Ser	Asn	Ser	Ala	Val	Asp	Gly	Thr	Ala	Gly	Pro	Gly
	225				230					235				240	
Ser	Ala	Ala	Thr	Leu	Asp	His	Asn	Gln	Pro	Tyr	His	Ile	Cys	Arg	Gly
			245					250					255		
Phe	Thr	Cys	Phe	Lys	Lys	Pro	Pro	Thr	Pro	Pro	Pro	Glu	Pro	Glu	Thr
			260					265					270		

&lt;210&gt; 27

&lt;211&gt; 840

&lt;212&gt; DNA

&lt;213&gt; Artificial sequence

&lt;220&gt;

&lt;223&gt; nucleic acid sequence for the CopGFP-NA3 variant

&lt;400&gt; 27

atggagagcg acgagagcgg cctgcccgcg atggagatcg agtgcgcgat caccggcacc

60

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ctgaacggcg tggagttcga gctggtgggc ggcggagagg gcacccccga gcagggccgc 120
atgaccaaca agatgaagag caccaagggc gccctgacct tcagccccta cctgctgagc 180
cacgtgatgg gctacgggtt ctaccacttc ggcaacctacc ccagcggcta cgagaacccc 240
ttcctgcacg ccatcaacaa cggcgggtac accaacaccc gcatacgagaa gtacgaggac 300
ggcggcgtgc tgcacgtgag cttcagctac cgtacgagg ccggccgcgt gatcggcgac 360
ttcaaggtgg tgggcaccgg cttccccgag gacagcgtga tcttcaccga caagatcacc 420
cgcagcaacg ccaccgtgga gcacctgcac cccatggggc ataacgtgct ggtgggcagc 480
ttcgccccga ccttcagcct gcgcgacggc ggctactaca gcttcgtggt ggacagccac 540
atgcacttca agagcggcat ccaccccagc atcctgcaga acggggggccc catgttcgcc 600
ttccgcccgc tggaggagct gcacagcaac accgagctgg gcatacgtga gtaccagcac 660
gccttcaaga ccccgatcgc attogccaga tccagagccc aggccagcaa ctccgcctg 720
gatggcacag ccggaccggg atcggccgcg actctagatc ataatcagcc ataccacatt 780
tgtagaggtt ttacttgctt taaaaaacct cccacacctc cccctgaacc tgaacataa 840

```

<210> 28

<211> 279

<212> PRT

<213> Artificial sequence

<220>

<223> amino acid sequence for the CopGFP-NA3 variant

<400> 28

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Met Glu Ser Asp Glu Ser Gly Leu Pro Ala Met Glu Ile Glu Cys Arg
1           5           10          15
Ile Thr Gly Thr Leu Asn Gly Val Glu Phe Glu Leu Val Gly Gly Gly
20          25          30
Glu Gly Thr Pro Glu Gln Gly Arg Met Thr Asn Lys Met Lys Ser Thr
35          40          45
Lys Gly Ala Leu Thr Phe Ser Pro Tyr Leu Leu Ser His Val Met Gly
50          55          60
Tyr Gly Phe Tyr His Phe Gly Thr Tyr Pro Ser Gly Tyr Glu Asn Pro
65          70          75          80
Phe Leu His Ala Ile Asn Asn Gly Gly Tyr Thr Asn Thr Arg Ile Glu
85          90          95
Lys Tyr Glu Asp Gly Gly Val Leu His Val Ser Phe Ser Tyr Arg Tyr
100         105         110
Glu Ala Gly Arg Val Ile Gly Asp Phe Lys Val Val Gly Thr Gly Phe
115         120         125
Pro Glu Asp Ser Val Ile Phe Thr Asp Lys Ile Ile Arg Ser Asn Ala
130         135         140

```

Thr Val Glu His Leu His Pro Met Gly Asp Asn Val Leu Val Gly Ser  
 145 150 155 160  
 Phe Ala Arg Thr Phe Ser Leu Arg Asp Gly Gly Tyr Tyr Ser Phe Val  
 165 170 175  
 Val Asp Ser His Met His Phe Lys Ser Ala Ile His Pro Ser Ile Leu  
 180 185 190  
 Gln Asn Gly Gly Pro Met Phe Ala Phe Arg Arg Val Glu Glu Leu His  
 195 200 205  
 Ser Asn Thr Glu Leu Gly Ile Val Glu Tyr Gln His Ala Phe Lys Thr  
 210 215 220  
 Pro Ile Ala Phe Ala Arg Ser Arg Ala Gln Ala Ser Asn Ser Ala Val  
 225 230 235 240  
 Asp Gly Thr Ala Gly Pro Gly Ser Ala Ala Thr Leu Asp His Asn Gln  
 245 250 255  
 Pro Tyr His Ile Cys Arg Gly Phe Thr Cys Phe Lys Lys Pro Pro Thr  
 260 265 270  
 Pro Pro Pro Glu Pro Glu Thr  
 275

&lt;210&gt; 29

&lt;211&gt; 238

&lt;212&gt; PRT

&lt;213&gt; Aequorea victoria

&lt;400&gt; 29

Met Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val  
 1 5 10 15  
 Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu  
 20 25 30  
 Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys  
 35 40 45  
 Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe  
 50 55 60  
 Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln  
 65 70 75 80  
 His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg  
 85 90 95  
 Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val  
 100 105 110  
 Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile

115	120	125
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn		
130	135	140
Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly		
145	150	155
Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val		
165	170	175
Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro		
180	185	190
Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser		
195	200	205
Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val		
210	215	220
Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys		
225	230	235

<210> 30  
 <211> 225  
 <212> PRT  
 <213> Discosoma sp.

<400> 30

Met Arg Ser Ser Lys Asn Val Ile Lys Glu Phe Met Arg Phe Lys Val		
1	5	10
Arg Met Glu Gly Thr Val Asn Gly His Glu Phe Glu Ile Glu Gly Glu		
20	25	30
Gly Glu Gly Arg Pro Tyr Glu Gly His Asn Thr Val Lys Leu Lys Val		
35	40	45
Thr Lys Gly Gly Pro Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln		
50	55	60
Phe Gln Tyr Gly Ser Lys Val Tyr Val Lys His Pro Ala Asp Ile Pro		
65	70	75
Asp Tyr Lys Lys Leu Ser Phe Pro Glu Gly Phe Lys Trp Glu Arg Val		
85	90	95
Met Asn Phe Glu Asp Gly Gly Val Val Thr Val Thr Gln Asp Ser Ser		
100	105	110
Leu Gln Asp Gly Cys Phe Ile Tyr Lys Val Lys Phe Ile Gly Val Asn		
115	120	125
Phe Pro Ser Asp Gly Pro Val-Met Gln Lys Lys Thr Met Gly Trp Glu		
130	135	140

[illegible]